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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,639A

DATE: 04/14/2003

TIME: 09:46:49

Input Set : N:\Crf4\04032003\J088639.raw
 Output Set: N:\CRF4\04142003\J088639A.raw

1 <110> APPLICANT: Brodin, Thomas
 2 Karlstrom, Pia J.
 3 Ohlsson, Lennart G.
 4 Tordsson, Jesper M.
 5 Kearney, Philip P.
 6 Nilson, Bo H.K.
 7 <120> TITLE OF INVENTION: Novel Compounds
 8 <130> FILE REFERENCE: 003300-920
 9 <140> CURRENT APPLICATION NUMBER: US/10/088,639A
C--> 10 <141> CURRENT FILING DATE: 1999-10-28
 11 <150> PRIOR APPLICATION NUMBER: SE 9903895-2
 12 <151> PRIOR FILING DATE: 1999-10-28
 13 <160> NUMBER OF SEQ ID NOS: 51
 14 <170> SOFTWARE: PatentIn Ver. 2.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 747
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Macaca fascicularis
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (1)..(747)
 22 <223> OTHER INFORMATION: Coding sequence VL (1-109) - modified Huston
 23 linker (110-127) - VH (128-249)
 24 <400> SEQUENCE: 1
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 26 tct tct gag ctg act cag ggc cct gca ttg tct gtg gcc ttg gga cat 48
 27 Ser Ser Glu Leu Thr Gln Gly Pro Ala Leu Ser Val Ala Leu Gly His
 28 1 5 10 15
 29 aca gtc agg atg acc tgc caa gga gac agc ctc aaa acc tat tat gca 96
 30 Thr Val Arg Met Thr Cys Gln Gly Asp Ser Leu Lys Thr Tyr Tyr Ala
 31 20 25 30
 32 agc tgg tac cag cag aag cca ggc cag gtc cct gtg ctg gtc atc tat 144
 33 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Val Leu Val Ile Tyr
 34 35 40 45
 35 ggt aac aac tac cgg ccc tca ggg atc cca ggc cga ttc tct ggc tcc 192
 36 Gly Asn Asn Tyr Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser Gly Ser
 37 50 55 60
 38 tgg tca gga aac aca gct tcc ttg acc atc act gcg gct cag gtg gaa 240
 39 Trp Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Ala Ala Gln Val Glu
 40 65 70 75 80
 41 gat gag gct gac tat tac tgt aac tcc tgg gac agc agc ggt acc cat 288
 42 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Trp Asp Ser Ser Gly Thr His
 43 85 90 95
 44 ccg gta ttc ggc gga ggg acc cgg gtg acc gtc cta ggt caa gcc aac 336

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45	Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu Gly Gln Ala Asn			
46	100	105	110	
47	ggt gaa ggc ggc tct ggt ggc ggg gga tcc gga ggc ggc ggt tct gag	384		
48	Gly Glu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly			
49	115	120	125	
50	gtg cag ttg gtg gag tct ggg gga ggc ttg gta aag cct ggg ggg tcc	432		
51	Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys Pro Gly Gly Ser			
52	130	135	140	
53	ctg aga ctc tct tgt gta gcc tct ggg tcc atc ttc agt agc tct gtt	480		
54	Leu Arg Leu Ser Cys Val Ala Ser Gly Ser Ile Phe Ser Ser Ser Val			
55	145	150	155	160
56	atg cac tgg gtc cgc cag gct cca gga aag ggt ctg gag tgg gtc tca	528		
57	Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser			
58	165	170	175	
59	gtt att agt gaa aat ggg cgt acc att aac tac gca gac tct gtg aag	576		
60	Val Ile Ser Glu Asn Gly Arg Thr Ile Asn Tyr Ala Asp Ser Val Lys			
61	180	185	190	
62	ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg ttt ctg	624		
63	Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu			
64	195	200	205	
65	cag atg aac agc ctg aca ggc gag gac acg gcc gtc tat tac tgt agt	672		
66	Gln Met Asn Ser Leu Thr Gly Glu Asp Thr Ala Val Tyr Tyr Cys Ser			
67	210	215	220	
68	aga gag ggg gga cct gga aca acg tcc aac cgg ctc gat gcc tgg ggc	720		
69	Arg Glu Gly Gly Pro Gly Thr Thr Ser Asn Arg Leu Asp Ala Trp Gly			
70	225	230	235	240
71	ccg gga gtc ctg gtc acc gtt tcc tca	747		
72	Pro Gly Val Leu Val Thr Val Ser Ser			
73	245			
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76	<211> LENGTH: 249			
77	<212> TYPE: PRT			
78	<213> ORGANISM: Macaca fascicularis			
79	<220> FEATURE:			
80	<223> OTHER INFORMATION: Coding sequence VL (1-109) - modified Huston			
81	linker (110-127) - VH (128-249)			
82	<400> SEQUENCE: 2			
83	Ser Ser Glu Leu Thr Gln Gly Pro Ala Leu Ser Val Ala Leu Gly His			
84	1	5	10	15
85	Thr Val Arg Met Thr Cys Gln Gly Asp Ser Leu Lys Thr Tyr Tyr Ala			
86	20	25	30	
87	Ser Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Val Leu Val Ile Tyr			
88	35	40	45	
89	Gly Asn Asn Tyr Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser Gly Ser			
90	50	55	60	
91	Trp Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Ala Ala Gln Val Glu			
92	65	70	75	80
93	Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Trp Asp Ser Ser Gly Thr His			
94	85	90	95	

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95 Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu Gly Gln Ala Asn
96          100           105           110
97 Gly Glu Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly
98          115           120           125
99 Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys Pro Gly Gly Ser
100         130           135           140
101 Leu Arg Leu Ser Cys Val Ala Ser Gly Ser Ile Phe Ser Ser Ser Val
102         145           150           155           160
103 Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
104         165           170           175
105 Val Ile Ser Glu Asn Gly Arg Thr Ile Asn Tyr Ala Asp Ser Val Lys
106         180           185           190
107 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu
108         195           200           205
109 Gln Met Asn Ser Leu Thr Gly Glu Asp Thr Ala Val Tyr Tyr Cys Ser
110         210           215           220
111 Arg Glu Gly Gly Pro Gly Thr Thr Ser Asn Arg Leu Asp Ala Trp Gly
112         225           230           235           240
113 Pro Gly Val Leu Val Thr Val Ser Ser
114         245

116 <210> SEQ ID NO: 3
117 <211> LENGTH: 1073
118 <212> TYPE: PRT
119 <213> ORGANISM: Human
120 <220> FEATURE:
121 <223> OTHER INFORMATION: TA6-Human integrin alpha-6A
122 <400> SEQUENCE: 3
123 Met Ala Ala Ala Gly Gln Leu Cys Leu Leu Tyr Leu Ser Ala Gly Leu
124          1           5           10           15
125 Leu Ser Arg Leu Gly Ala Ala Phe Asn Leu Asp Thr Arg Glu Asp Asn
126          20          25           30
127 Val Ile Arg Lys Tyr Gly Asp Pro Gly Ser Leu Phe Gly Phe Ser Leu
128          35          40           45
129 Ala Met His Trp Gln Leu Gln Pro Glu Asp Lys Arg Leu Leu Leu Val
130          50          55           60
131 Gly Ala Pro Arg Gly Glu Ala Leu Pro Leu Gln Arg Ala Asn Arg Thr
132          65          70           75           80
133 Gly Gly Leu Tyr Ser Cys Asp Ile Thr Ala Arg Gly Pro Cys Thr Arg
134          85          90           95
135 Ile Glu Phe Asp Asn Asp Ala Asp Pro Thr Ser Glu Ser Lys Glu Asp
136          100         105           110
137 Gln Trp Met Gly Val Thr Val Gln Ser Gln Gly Pro Gly Gly Lys Val
138          115         120           125
139 Val Thr Cys Ala His Arg Tyr Glu Lys Arg Gln His Val Asn Thr Lys
140          130         135           140
141 Gln Glu Ser Arg Asp Ile Phe Gly Arg Cys Tyr Val Leu Ser Gln Asn
142          145         150           155           160
143 Leu Arg Ile Glu Asp Asp Met Asp Gly Gly Asp Trp Ser Phe Cys Asp
144          165         170           175

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145 Gly Arg Leu Arg Gly His Glu Lys Phe Gly Ser Cys Gln Gln Gly Val
 146 180 185 190
 147 Ala Ala Thr Phe Thr Lys Asp Phe His Tyr Ile Val Phe Gly Ala Pro
 148 195 200 205
 149 Gly Thr Tyr Asn Trp Lys Gly Ile Val Arg Val Glu Gln Lys Asn Asn
 150 210 215 220
 151 Thr Phe Phe Asp Met Asn Ile Phe Glu Asp Gly Pro Tyr Glu Val Gly
 152 225 230 235 240
 153 Gly Glu Thr Glu His Asp Glu Ser Leu Val Pro Val Pro Ala Asn Ser
 154 245 250 255
 155 Tyr Leu Gly Phe Ser Leu Asp Ser Gly Lys Gly Ile Val Ser Lys Asp
 156 260 265 270
 157 Glu Ile Thr Phe Val Ser Gly Ala Pro Arg Ala Asn His Ser Gly Ala
 158 275 280 285
 159 Val Val Leu Leu Lys Arg Asp Met Lys Ser Ala His Leu Leu Pro Glu
 160 290 295 300
 161 His Ile Phe Asp Gly Glu Gly Leu Ala Ser Ser Phe Gly Tyr Asp Val
 162 305 310 315 320
 163 Ala Val Val Asp Leu Asn Lys Asp Gly Trp Gln Asp Ile Val Ile Gly
 164 325 330 335
 165 Ala Pro Gln Tyr Phe Asp Arg Asp Gly Glu Val Gly Gly Ala Val Tyr
 166 340 345 350
 167 Val Tyr Met Asn Gln Gln Gly Arg Trp Asn Asn Val Lys Pro Ile Arg
 168 355 360 365
 169 Leu Asn Gly Thr Lys Asp Ser Met Phe Gly Ile Ala Val Lys Asn Ile
 170 370 375 380
 171 Gly Asp Ile Asn Gln Asp Gly Tyr Pro Asp Ile Ala Val Gly Ala Pro
 172 385 390 395 400
 173 Tyr Asp Asp Leu Gly Lys Val Phe Ile Tyr His Gly Ser Ala Asn Gly
 174 405 410 415
 175 Ile Asn Thr Lys Pro Thr Gln Val Leu Lys Gly Ile Ser Pro Tyr Phe
 176 420 425 430
 177 Gly Tyr Ser Ile Ala Gly Asn Met Asp Leu Asp Arg Asn Ser Tyr Pro
 178 435 440 445
 179 Asp Val Ala Val Gly Ser Leu Ser Asp Ser Val Thr Ile Phe Arg Ser
 180 450 455 460
 181 Arg Pro Val Ile Asn Ile Gln Lys Thr Ile Thr Val Thr Pro Asn Arg
 182 465 470 475 480
 183 Ile Asp Leu Arg Gln Lys Thr Ala Cys Gly Ala Pro Ser Gly Ile Cys
 184 485 490 495
 185 Leu Gln Val Lys Ser Cys Phe Glu Tyr Thr Ala Asn Pro Ala Gly Tyr
 186 500 505 510
 187 Asn Pro Ser Ile Ser Ile Val Gly Thr Leu Glu Ala Glu Lys Glu Arg
 188 515 520 525
 189 Arg Lys Ser Gly Leu Ser Ser Arg Val Gln Phe Arg Asn Gln Gly Ser
 190 530 535 540
 191 Glu Pro Lys Tyr Thr Gln Glu Leu Thr Leu Lys Arg Gln Lys Gln Lys
 192 545 550 555 560
 193 Val Cys Met Glu Glu Thr Leu Trp Leu Gln Asp Asn Ile Arg Asp Lys

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194	565	570	575	
195	Leu Arg Pro Ile Pro Ile Thr Ala Ser Val Glu Ile Gln Glu Pro Ser			
196	580	585	590	
197	Ser Arg Arg Arg Val Asn Ser Leu Pro Glu Val Leu Pro Ile Leu Asn			
198	595	600	605	
199	Ser Asp Glu Pro Lys Thr Ala His Ile Asp Val His Phe Leu Lys Glu			
200	610	615	620	
201	Gly Cys Gly Asp Asp Asn Val Cys Asn Ser Asn Leu Lys Leu Glu Tyr			
202	625	630	635	640
203	Lys Phe Cys Thr Arg Glu Gly Asn Gln Asp Lys Phe Ser Tyr Leu Pro			
204	645	650	655	
205	Ile Gln Lys Gly Val Pro Glu Leu Val Leu Lys Asp Gln Lys Asp Ile			
206	660	665	670	
207	Ala Leu Glu Ile Thr Val Thr Asn Ser Pro Ser Asn Pro Arg Asn Pro			
208	675	680	685	
209	Thr Lys Asp Gly Asp Asp Ala His Glu Ala Lys Leu Ile Ala Thr Phe			
210	690	695	700	
211	Pro Asp Thr Leu Thr Tyr Ser Ala Tyr Arg Glu Leu Arg Ala Phe Pro			
212	705	710	715	720
213	Glu Lys Gln Leu Ser Cys Val Ala Asn Gln Asn Gly Ser Gln Ala Asp			
214	725	730	735	
215	Cys Glu Leu Gly Asn Pro Phe Lys Arg Asn Ser Asn Val Thr Phe Tyr			
216	740	745	750	
217	Leu Val Leu Ser Thr Thr Glu Val Thr Phe Asp Thr Pro Asp Leu Asp			
218	755	760	765	
219	Ile Asn Leu Lys Leu Glu Thr Thr Ser Asn Gln Asp Asn Leu Ala Pro			
220	770	775	780	
221	Ile Thr Ala Lys Ala Lys Val Val Ile Glu Leu Leu Leu Ser Val Ser			
222	785	790	795	800
223	Gly Val Ala Lys Pro Ser Gln Val Tyr Phe Gly Gly Thr Val Val Gly			
224	805	810	815	
225	Glu Gln Ala Met Lys Ser Glu Asp Glu Val Gly Ser Leu Ile Glu Tyr			
226	820	825	830	
227	Glu Phe Arg Val Ile Asn Leu Gly Lys Pro Leu Thr Asn Leu Gly Thr			
228	835	840	845	
229	Ala Thr Leu Asn Ile Gln Trp Pro Lys Glu Ile Ser Asn Gly Lys Trp			
230	850	855	860	
231	Leu Leu Tyr Leu Val Lys Val Glu Ser Lys Gly Leu Glu Lys Val Thr			
232	865	870	875	880
233	Cys Glu Pro Gln Lys Glu Ile Asn Ser Leu Asn Leu Thr Glu Ser His			
234	885	890	895	
235	Asn Ser Arg Lys Lys Arg Glu Ile Thr Glu Lys Gln Ile Asp Asp Asn			
236	900	905	910	
237	Arg Lys Phe Ser Leu Phe Ala Glu Arg Lys Tyr Gln Thr Leu Asn Cys			
238	915	920	925	
239	Ser Val Asn Val Asn Cys Val Asn Ile Arg Cys Pro Leu Arg Gly Leu			
240	930	935	940	
241	Asp Ser Lys Ala Ser Leu Ile Leu Arg Ser Arg Leu Trp Asn Ser Thr			
242	945	950	955	960

VERIFICATION SUMMARY

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Input Set : N:\Crf4\04032003\J088639.raw
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date